

11420122.APP
SEQUENCE LISTING

<110> Pausch, Mark H
Price, Laura A

<120> POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM, AND METHODS OF USING SAME

<130> 01142.0122 SEQUENCE LISTING

<140> 08/816,011
<141> 1997-03-11

<150> 07/332,312
<151> 1994-10-31

<150> PCT/US95/14364
<151> 1995-10-25

<160> 67

<170> PatentIn Ver. 2.1

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<212> DNA
<213> Drosophila melanogaster

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<212> PRT

<213> Drosophila melanogaster

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Gly	Ile	Pro	Val	Asn	Gly	Ile	Leu	Phe	Ala	Gly	Leu	Gly	Glu	Tyr	Phe
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Gly	Arg	Thr	Phe	Glu	Ala	Ile	Tyr	Arg	Arg	Tyr	Lys	Lys	Tyr	Lys	Met
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Ser	Thr	Asp	Met	His	Tyr	Val	Pro	Pro	Gln	Leu	Gly	Leu	Ile	Thr	Thr
						165			170			175			

Val	Val	Ile	Ala	Leu	Ile	Pro	Gly	Ile	Ala	Leu	Phe	Leu	Val	Leu	Pro
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Cys	Val	Gly	Val	His	Leu	Leu	Arg	Glu	Leu	Gly	Leu	Ser	Ser	Ile	Ser
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Val	Pro	Thr	Phe	Gly	Ala	Asn	Gln	Pro	Lys	Glu	Phe	Gly	Gly	Trp	Phe
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Val	Val	Tyr	Gln	Ile	Phe	Val	Ile	Val	Trp	Phe	Ile	Phe	Ser	Leu	Gly
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Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr
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Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg
290 295 300

Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr
305 310 315 320

Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp
325 330 335

Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg
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Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly
355 360 365

Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu
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Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
385 390 395 400

Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
405 410 415

Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
420 425 430

Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
435 440 445

Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
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Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
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Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln
485 490 495

Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
500 505 510

Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
515 520 525

Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
530 535 540

Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala
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Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
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Asp Pro Arg Trp Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
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 tcaatgaaaa aaaaacaaaa attcaaaaata ttttttagtc ttgcaataac tacaatgtgc 660
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Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
 35 40 45

Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
 50 55 60

Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly
 65 70 75 80

Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
 85 90 95

Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
 100 105 110

Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
 115 120 125

Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val

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130

135

140

Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
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Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
165 170 175

Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
180 185 190

Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe
195 200 205

Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
210 215 220

Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
225 230 235 240

Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val
245 250 255

Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
260 265 270

Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
275 280 285

Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
290 295 300

Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ala Ile Asp Met Gln
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<211> 24

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<213> Drosophila melanogaster

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<211> 24

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<213> Drosophila melanogaster

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Ile Ser Pro Thr Thr Phe Ala Gly
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<213> Drosophila melanogaster

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 <213> Drosophila melanogaster

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Tyr Val Pro Thr Phe Gly Ala Asn
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<213> Drosophila melanogaster

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<210> 31

<211> 24

<212> DNA

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<213> Drosophila melanogaster

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<212> DNA

<213> Drosophila melanogaster

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<210> 36
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 <213> *Caenorhabditis elegans*

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 <213> *Drosophila melanogaster*

<400> 37

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		20				25			30						
Lys	Ile	Ser	Arg	Ala	Glu	Gln	Arg	Lys	Ala	Gln	Ile	Ala	Ile	Asn	Glu
		35			40				45						
Tyr	Leu	Leu	Glu	Glu	Leu	Gly	Asp	Lys	Asn	Thr	Thr	Thr	Gln	Asp	Glu
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Pro	Thr	Tyr	Asp	Asp	Thr	Pro	Tyr	Thr	Trp	Thr	Phe	Tyr	His	Ala	Phe
		85			90										95
Phe	Phe	Ala	Phe	Thr	Val	Cys	Ser	Thr	Val	Gly	Tyr	Gly	Asn	Ile	Ser
		100			105										110
Pro	Thr	Thr	Phe	Ala	Gly	Arg	Met	Ile	Met	Ile	Ala	Tyr	Ser	Val	Ile

115

120

125

Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe
 130 135 140

Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met
 145 150 155 160

Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr
 165 170 175

Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro
 180 185 190

Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser
 195 200 205

Leu Tyr Tyr Ser Tyr Val Thr Ile Thr Thr Ile Gly Phe Gly Asp Tyr
 210 215 220

Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe
 225 230 235 240

Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly
 245 250 255

Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys
 260 265 270

Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr
 275 280 285

Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg
 290 295 300

Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr
 305 310 315 320

Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp
 325 330 335

Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg
 340 345 350

Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly
 355 360 365

Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu
 370 375 380

Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
 385 390 395 400

Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
 405 410 415

Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
 420 425 430

Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
 435 440 445

Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
 Page 12

450

455

460

Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
 465 470 475 480

Trp

<210> 38
 <211> 337
 <212> PRT
 <213> *Caenorhabditis elegans*

<220>
 <221> UNSURE
 <222> (337)
 <223> X AT RESIDUE 337 IS AN UNKNOWN RESIDUE

<400> 38
 Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser
 1 5 10 15

Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser
 20 25 30

Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
 35 40 45

Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
 50 55 60

Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Cys Leu Ala Gly
 65 70 75 80

Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
 85 90 95

Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
 100 105 110

Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
 115 120 125

Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
 130 135 140

Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
 145 150 155 160

Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
 165 170 175

Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
 180 185 190

Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe
 195 200 205

Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
 210 215 220

Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
 Page 13

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225	230	235	240
Asp Ala Arg Ser Ala	Leu Ala Val Val	Gly Gly Lys Val Val	Leu Val
245	250	255	
Ser Glu Leu Tyr Ala Asn Leu Met	Gln Lys Arg Ala Arg Asn Met Ser		
260	265	270	
Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile			
275	280	285	
Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr			
290	295	300	
Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ala Ile Asp Met Gln			
305	310	315	320
Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys			
325	330	335	

Xaa

<210> 39
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DEGENERATE
PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<220>
<221> variation
<222> (2)
<223> N AT BASE 2 INDICATES ANY NUCLEOTIDE

<400> 39
tnggatwygg wgaywyt 17

<210> 40
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DEGENERATE
PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<400> 40
rtcwccrwah ccdaydgt 18

<210> 41
<211> 28
<212> DNA
<213> Homo sapiens

<400> 41
cgcaggcaga gccacaaaga gtacacag 28

<210> 42
 <211> 26
 <212> DNA
 <213> Homo sapiens

<400> 42
 ggagatcagc taggcaccat atttgg

26

<210> 43
 <211> 26
 <212> DNA
 <213> Homo sapiens

<400> 43
 atgctgcattg cctcatgctt cccagc

26

<210> 44
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 44
 gtttatttaa agagagggct

20

<210> 45
 <211> 426
 <212> PRT
 <213> Homo sapiens

<400> 45
 Met Leu Pro Ser Ala Ser Arg Glu Arg Pro Gly Tyr Arg Ala Gly Val
 1 5 10 15
 Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser Lys
 20 25 30
 Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg Val
 35 40 45
 Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser Thr
 50 55 60
 Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val Phe
 65 70 75 80
 Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile Val
 85 90 95
 Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser Thr
 100 105 110
 Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala Gly
 115 120 125
 Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp Leu
 130 135 140
 Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly Phe
 145 150 155 160

11420122.APP

Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile Ile
165 170 175

Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly Val
180 185 190

Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val Glu
195 200 205

Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile Ile
210 215 220

Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala Leu
225 230 235 240

Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp Ala
245 250 255

Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr
260 265 270

Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro Val
275 280 285

Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu
290 295 300

Ser Met Ile Gly Arg Leu Val Arg Val Ile Ser Lys Lys Thr Lys Glu
305 310 315 320

Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn Val
325 330 335

Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile Tyr
340 345 350

Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala Glu
355 360 365

Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr Leu
370 375 380

Ser Val Asn His Leu Thr Ser Glu Arg Asp Val Leu Pro Pro Leu Leu
385 390 395 400

Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Ala Pro His Cys Ala Gly
405 410 415

Glu Glu Ile Ala Val Ile Glu Asn Ile Lys
420 425

<210> 46
<211> 2130
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (35)
<223> N AT POSITION 35 INDICATES UNDETERMINED
NUCLEOTIDE

<220>
 <221> unsure
 <222> (2057)
 <223> N AT POSITION 2057 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2067)
 <223> N AT POSITION 2067 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2111)
 <223> N AT POSITION 2111 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2120)
 <223> N AT POSITION 2120 INDICATES UNDETERMINED
 NUCLEOTIDE

<400> 46

ccatccta	at	acgactca	act	atagggctcg	agcgnccgc	cgggcagtaa	aatgcctgcc	60			
cgtcagctc	ggagcgcgc	ca	gcccgtct	ct	gaataaga	tgagtaca	at	ggcgtgtt	120		
taaaaaaaag	cttcaag	ttc	gtcttt	ca	aaaaacattt	tgaatgctgc	at	gcctcatg	180		
cttcccagcg	cctc	cgccg	gagacccggc	gag	tatagagcag	gagtggcggc	ac	ctgactt	240		
ctggatccta	aat	ctgc	ccgc	tc	agaactcc	aaaccgaggc	tctc	at	tcgaaaccc	300	
acagtgc	ttt	ccc	ggg	gt	ggagagt	gac	acgaccat	at	ttatgaa	360	
gtctccacga	tat	tcc	tgt	gt	ttgtgc	ctc	tatctgatc	tc	ggagccac	420	
gcattggagc	agc	ctc	at	ca	tttccacag	agg	accacca	tt	gtatcca	480	
ttcatatccc	aa	cattcct	tg	tca	attcg	ac	ggagctt	at	gaaactcat	540	
gtggcagcaa	taa	atgc	cagg	gat	tataccg	t	taggaa	ac	tc	caata	600
tgggatttgg	gaag	ttc	ctt	ctt	gt	gg	ca	t	ttacaaccat	aggattt	660
aacatctcac	cac	gcac	aga	gg	ccgca	aa	atattctgt	t	catctatgc	cttactt	720
attccccct	ttg	ttt	ttc	ct	tg	gg	gat	ag	ttaggcac	catattt	780
aaaggaaattt	ccaa	agg	atgt	g	gat	ac	ttaa	at	tttagtca	gaccaagat	840
cgcacatcat	ca	aca	atcat	at	tata	act	tttggctgt	tac	tctttgt	ggctctgc	900
gcatcatat	tca	aa	acat	aca	at	agg	gttgc	ac	gcattt	ttttgt	960
atcactctaa	ca	act	attt	gg	tgt	gac	tac	gt	ggatccg	tattgaat	1020
ctggacttct	at	a	agg	c	tg	tgc	tg	tg	ggatccg	ttacttt	1080
gctgtcctga	gc	at	tg	at	ttt	gg	tgat	tt	ggctt	aaaagaagag	1140
gtgggagagt	tca	ag	ag	ca	cg	tgt	gat	ct	tttttt	ttttgt	1200
gaaaccagga	gg	gc	act	g	tg	tg	gat	t	tttttt	tttttt	1260
aagcggaa	tct	ccg	caga	act	gg	cttgc	tttttt	tt	tttttt	tttttt	1320
aggaccctgt	c	at	gt	g	tttgc	tttttt	tttttt	tt	tttttt	tttttt	1380
actgagagta	tct	at	ctgt	aa	tttgc	tttttt	tttttt	tt	tttttt	tttttt	1440
attgagaaca	tca	aa	atag	cc	tttgc	tttttt	tttttt	tt	tttttt	tttttt	1500
ttctctatgc	tct	ttt	atgc	tgc	tttgc	tttttt	tttttt	tt	tttttt	tttttt	1560
ggggaa	aa	at	agat	aca	tttgc	tttttt	tttttt	tt	tttttt	tttttt	1620
gagccagcac	ttt	ctt	ttt	ctg	tttgc	tttttt	tttttt	tt	tttttt	tttttt	1680
atgacaagca	at	gt	ctgt	at	tttgc	tttttt	tttttt	tt	tttttt	tttttt	1740
tgtgcataa	gg	cc	tc	gaa	tttgc	tttttt	tttttt	tt	tttttt	tttttt	1800
gatcgttct	taa	c	ctt	ttt	tttgc	tttttt	tttttt	tt	tttttt	tttttt	1860
tgacaacaat	ttt	ttt	ttt	ttt	tttgc	tttttt	tttttt	tt	tttttt	tttttt	1920
atttctgtca	gt	gc	ttt	tat	tttgc	tttttt	tttttt	tt	tttttt	tttttt	1980
tccttccctg	cccc	cccc	cccc	cc	tttgc	tttttt	tttttt	tt	tttttt	tttttt	2040
tgaataccat	ac	ctt	gtt	gtt	tttgc	tttttt	tttttt	tt	tttttt	tttttt	2100
gaaatagatg	nc	aa	att	tg	tttgc	tttttt	tttttt	tt	tttttt	tttttt	2130

<210> 47
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 47
 aaaagatcta aaatgcttcc cagcgcc

27

<210> 48
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 48
 aaagtcgacc tatttgatgt tctcaat

27

<210> 49
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 49
 aaaaagctta aaatgcttcc cagcgcc

27

<210> 50
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 50
 aaatctagac tatttgatgt tctcaat

27

<210> 51
 <211> 534
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (262)
 <223> N AT POSITION 262 INDICATES UNDETERMINED
 NUCLEOTIDE

<400> 51
 aacaaaaaacc tttttgttt tgaatggcct agagaggta agggatcccc tgacgaacag 60
 gagcagagcc agctagaacc tggcctggc cagttcaagg ccaccagagg gcagccttct 120
 gcggaaggca gtattgggtt aggcaggac cccagcagac atggcactca gagctctcac 180
 tgtccactga ctctctcttc tccaggttat ggcacatgg cccactatc gccaggcgga 240
 aaggccttct gcatggtctt antagccctt gggctgccag cctccttagc tctcgtggcc 300
 accctgcgcc attgcctgct gcctgtgctc agccgcccac gtgcctgggt agcggtccac 360
 tggcagctgt caccggccag ggctgcgtg ctgcaggcag ttgcactggg actgctgggt 420
 gccagcagct ttgtgctgct gccagcgtg gtgctgtggg gccttcaggg cgactgcagc 480
 ctgctggggg ccgtctactt ctgcttcagc tcgctcagca ccattggcct gggg 534

<210> 52
 <211> 956
 <212> DNA

<213> Mus musculus

<400> 52

atgatacgt	ttaatacgtac	tcactatagg	gaatttggcc	ctcgaggcca	agaattcgcc	60
acgaggagaa	tgtgcgcacg	ttggctctca	tcgtgtgcac	cttcacctac	ctgctggtgg	120
gcccgcgt	tttcgcacgca	ctggagtcgg	agccggagat	gatcgagcgg	cagcggctgg	180
agctgcggca	gctggagctg	cgggcgcgt	acaacctcag	cgagggcggc	tacgaggagc	240
tggagcgcgt	cgtgtgcgc	ctcaagccgc	acaaggccgg	cgtgcagtgg	cgcttcgcgg	300
gctccctcta	tttcgcgcatt	accgtcatca	ccaccatcg	ctatggtcat	gcggcgcccc	360
gcacgacgg	aggcaagggt	ttctgcatgt	tctacgcgt	gctgggcatt	ccgctcacac	420
tagtcatgtt	ccagagcctg	ggtgaacgca	tcaacaccc	cgtgaggtac	ctgctgcacc	480
gtgccaagag	ggggctgggc	atgcggcag	ccgaagtgtc	catggcaac	atggtgccta	540
tcggtttgcgt	gtcgtgcattc	agcacgctgt	gcacgcgc	agctgccttc	tcctactacg	600
agcgctggac	tttcttccag	gcctattact	actgcttcat	caccctcacc	accatcggt	660
tcggcacta	tgtggcgctg	cagaaggacc	aggcgctgca	gacgcagccg	cagtatgtgg	720
cttcagcttc	gtgtacatcc	tcacgggctc	acggtcatcg	gcgccttc	aacctcgtgg	780
tgctgcgatt	catgaccatg	aacgcccagg	acgagaagcg	tgtatgcggag	caccgcgc	840
tgctcagcga	caacggccag	gctgtcgcc	tgggtggct	gagctgcctg	agcggtagcc	900
tggcgacgg	cgtgcgtccc	cgcgaccagg	tcacatgcgc	tgccggccgca	agctta	956

<210> 53

<211> 1055

<212> DNA

<213> Mus musculus

<220>

<221> unsure

<222> (247)

<223> N AT POSITION 247 INDICATES UNDETERMINED NUCLEOTIDE

<220>

<221> unsure

<222> (593)

<223> N AT POSITION 593 INDICATES UNDETERMINED NUCLEOTIDE

<220>

<221> unsure

<222> (952)

<223> N AT POSITION 952 INDICATES UNDETERMINED NUCLEOTIDE

<400> 53

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ggggctgtgg	tgcttcagggc	cctggagggc	cctccagctc	gccacctcca	ggcccaggtc	120
caggctgaac	ttggcttagctt	ccaggcagag	cacagggcct	gcttgcacc	tgaggccctg	180
gaggagctgc	taggtgcgg	cctgagagca	caggcccatt	gagttccag	cctggcaac	240
agctcanaga	caagcaactg	ggatctgccc	tcagctctgc	tgttcactgc	cagcatcc	300
accaccaccc	gttatggcca	catggccca	ctctcctcag	gtggaaaggc	cttctgtgt	360
gtctatgcag	cccttgggt	gccagcctct	ctagcacctg	tggctgcct	gcgcactgc	420
ttgctgcctg	tgttcagtcg	cccaggtgac	tgggttagcca	ttcgctggca	gctggcacca	480
gctcaggctg	ctctgctaca	ggcagcagga	ctggggctcc	tggggcctg	tgtttcatg	540
ctgctgccc	cactgggtct	gtgggggtgt	cagggtgact	ggcagcctgc	tanaaccatc	600
tacttctgtt	tcggctcact	cagcacgtc	ggccttaggg	acttgcgtcc	tgcccatgga	660
cgtggcctgc	accacgccc	ttaccaccc	gggcagttt	cacttcttgg	ttacttgc	720
ctggggctcc	tggccatgtt	gttagcaga	gagacccctt	cagactgccc	tcaggccgt	780
gccatggta	atttcttgg	gcccagtggc	tctagaaccg	atgaagatca	agatggc	840
ctagggcaag	atgagctg	tctgagact	gtgctgcctg	acgccccagt	cttgggacca	900
accacccag	cctgagcggg	aggcaccaag	gagtgcgtt	agaacatagc	angaaagggtt	960
atggaaatga	atatgtcatg	ggataatgtt	attttaaaaa	attaaatggg	ctgcttagca	1020
tgcaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaa			1055

<210> 54
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (88)
 <223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 54
 Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser
 1 5 10 15
 Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe
 20 25 30
 Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly
 35 40 45
 Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr
 50 55 60
 Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
 65 70 75 80
 Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
 85 90 95
 Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
 100 105 110
 Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
 115 120 125
 Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
 130 135 140
 Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
 145 150 155 160
 Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
 165 170 175
 Leu Gly

<210> 55
 <211> 309
 <212> PRT
 <213> Mus musculus

<400> 55
 Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
 1 5 10 15
 Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
 20 25 30
 Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln

35

40

45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser
 50 55 60

Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro
 65 70 75 80

His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala
 85 90 95

Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr
 100 105 110

Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro
 115 120 125

Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser
 130 135 140

Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His
 145 150 155 160

Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys
 165 170 175

Ile Ser Thr Leu Cys Ile Gly Ala Ala Phe Ser Tyr Tyr Glu Arg
 180 185 190

Trp Thr Phe Phe Gln Ala Tyr Tyr Cys Phe Ile Thr Leu Thr Thr
 195 200 205

Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln
 210 215 220

Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala
 225 230 235 240

His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr
 245 250 255

Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu
 260 265 270

Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser
 275 280 285

Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala
 290 295 300

Ala Ala Ala Ser Leu
 305

<210> 56

<211> 304

<212> PRT

<213> Mus musculus

<220>

<221> UNSURE

<222> (83)

<223> N AT POSITION 83 INDICATES UNDETERMINED RESIDUE

<220>

<221> UNSURE

<222> (198)

<223> N AT POSITION 198 INDICATES UNDETERMINED RESIDUE

<400> 56

Leu	Lys	Pro	Trp	Ala	Arg	Tyr	Leu	Leu	Leu	Leu	Met	Ala	His	Leu	Leu
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							25						30		
Ala	Arg	His	Leu	Gln	Ala	Gln	Val	Gln	Ala	Glu	Leu	Ala	Ser	Phe	Gln
							40						45		
Ala	Glu	His	Arg	Ala	Cys	Leu	Pro	Pro	Glu	Ala	Leu	Glu	Glu	Leu	Leu
						50						60			
Gly	Ala	Val	Leu	Arg	Ala	Gln	Ala	His	Gly	Val	Ser	Ser	Leu	Gly	Asn
						65				75					80
Ser	Ser	Xaa	Thr	Ser	Asn	Trp	Asp	Leu	Pro	Ser	Ala	Leu	Leu	Phe	Thr
						85			90					95	
Ala	Ser	Ile	Leu	Thr	Thr	Thr	Gly	Tyr	Gly	His	Met	Ala	Pro	Leu	Ser
						100			105				110		
Ser	Gly	Gly	Lys	Ala	Phe	Cys	Val	Val	Tyr	Ala	Ala	Leu	Gly	Leu	Pro
						115			120				125		
Ala	Ser	Leu	Ala	Leu	Val	Ala	Ala	Leu	Arg	His	Cys	Leu	Leu	Pro	Val
						130			135			140			
Phe	Ser	Arg	Pro	Gly	Asp	Trp	Val	Ala	Ile	Arg	Trp	Gln	Leu	Ala	Pro
						145			150			155			160
Ala	Gln	Ala	Ala	Leu	Leu	Gln	Ala	Ala	Gly	Leu	Gly	Leu	Leu	Val	Ala
						165			170				175		
Cys	Val	Phe	Met	Leu	Leu	Pro	Ala	Leu	Val	Leu	Trp	Gly	Val	Gln	Gly
						180			185			190			
Asp	Trp	Gln	Pro	Ala	Xaa	Thr	Ile	Tyr	Phe	Cys	Phe	Gly	Ser	Leu	Ser
						195			200			205			
Thr	Ile	Gly	Leu	Gly	Asp	Leu	Leu	Pro	Ala	His	Gly	Arg	Gly	Leu	His
						210			215			220			
Pro	Ala	Ile	Tyr	His	Leu	Gly	Gln	Phe	Ala	Leu	Leu	Gly	Tyr	Leu	Leu
						225			230			235			240
Leu	Gly	Leu	Leu	Ala	Met	Leu	Leu	Ala	Val	Glu	Thr	Phe	Ser	Glu	Leu
						245			250				255		
Pro	Gln	Val	Arg	Ala	Met	Val	Lys	Phe	Phe	Gly	Pro	Ser	Gly	Ser	Arg
						260			265			270			
Thr	Asp	Glu	Asp	Gln	Asp	Gly	Ile	Leu	Gly	Gln	Asp	Glu	Leu	Ala	Leu
						275			280			285			
Ser	Thr	Val	Leu	Pro	Asp	Ala	Pro	Val	Leu	Gly	Pro	Thr	Thr	Pro	Ala
						290			295			300			

<210> 57

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (1)..(9)

<223> X AT POSITIONS 1, 4, AND 5 IS T OR S; X AT POSITION 6 IS I OR V; X AT POSITIONS 2, 3, AND 8 IS Y, F, V, I, M, OR L

<220>

<223> Description of Artificial Sequence: POTASSIUM ION CHANNEL SEQUENCE

<400> 57

Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly
1 5

<210> 58

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (1)..(8)

<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A, S, OR G; X AT POSITIONS 3, 4, 6, AND 8 ARE M, I, V, L, F, OR Y

<400> 58

Xaa Xaa Xaa Xaa Gly Xaa Pro Xaa
1 5

<210> 59

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION CHANNEL SEQUENCE

<400> 59

Tyr Ala Leu Leu Gly Ile Pro
1 5

<210> 60

<211> 7

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: POTASSIUM ION
 CHANNEL SEQUENCE

<220>
 <221> VARIANT
 <222> (6)
 <223> X AT POSITION 6 IS M, I, V, L, F, OR Y

<400> 60
 Tyr Ala Leu Leu Gly Xaa Pro
 1 5

<210> 61
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (88)
 <223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 61
 Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser
 1 5 10 15
 Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe
 20 25 30
 Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly
 35 40 45
 Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr
 50 55 60
 Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
 65 70 75 80
 Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
 85 90 95
 Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
 100 105 110
 Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
 115 120 125
 Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
 130 135 140
 Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
 145 150 155 160
 Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
 165 170 175
 Leu Gly

<210> 62
 <211> 309
 <212> PRT
 <213> Mus musculus

<400> 62
 Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
 1 5 10 15
 Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
 20 25 30
 Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln
 35 40 45
 Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser
 50 55 60
 Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro
 65 70 75 80
 His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala
 85 90 95
 Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr
 100 105 110
 Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro
 115 120 125
 Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser
 130 135 140
 Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His
 145 150 155 160
 Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys
 165 170 175
 Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg
 180 185 190
 Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr
 195 200 205
 Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln
 210 215 220
 Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala
 225 230 235 240
 His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr
 245 250 255
 Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu
 260 265 270
 Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser
 275 280 285
 Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala

Ala Ala Ala Ser Leu
305

<210> 63

<211> 434

<212> PRT

<213> *Caenorhabditis elegans*

<400> 63

Met Val Ile Ile Asn Arg Ser Asn Thr Tyr Ala Val Glu Gln Glu Ala
1 5 10 15

Phe Pro Arg Asp Lys Tyr Asn Ile Val Tyr Trp Leu Val Ile Leu Val
20 25 30

Gly Phe Gly Val Leu Leu Pro Trp Asn Met Phe Ile Thr Ile Ala Pro
35 40 45

Glu Tyr Tyr Val Asn Tyr Trp Phe Lys Pro Asp Gly Val Glu Thr Trp
50 55 60

Tyr Ser Lys Glu Phe Met Gly Ser Leu Thr Ile Gly Ser Gln Leu Pro
65 70 75 80

Asn Ala Ser Ile Asn Val Phe Asn Leu Phe Leu Ile Ile Ala Gly Pro
85 90 95

Leu Ile Tyr Arg Val Phe Ala Pro Val Cys Phe Asn Ile Val Asn Leu
100 105 110

Thr Ile Ile Leu Ile Leu Val Ile Val Leu Glu Pro Thr Glu Asp Ser
115 120 125

Met Ser Trp Phe Phe Trp Val Thr Leu Gly Met Ala Thr Ser Ile Asn
130 135 140

Phe Ser Asn Gly Leu Tyr Glu Asn Ser Val Tyr Gly Val Gly Gly Asp
145 150 155 160

Phe Pro His Thr Tyr Ile Gly Ala Leu Leu Ile Gly Asn Asn Ile Cys
165 170 175

Gly Leu Leu Ile Thr Val Val Lys Ile Gly Val Thr Tyr Phe Leu Asn
180 185 190

Asp Glu Pro Lys Leu Val Ala Ile Val Tyr Phe Gly Ile Ser Leu Val
195 200 205

Ile Leu Leu Val Cys Ala Ile Ala Leu Phe Phe Ile Thr Lys Gln Asp
210 215 220

Phe Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala
225 230 235 240

Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu Trp Thr Thr Phe Thr Asn
245 250 255

Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu
260 265 270

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Thr Ile Phe Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly
275 280 285

Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile Tyr Thr Leu Leu
290 295 300

Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val
305 310 315 320

Ala Ser Lys Ile His Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile
325 330 335

Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Cys Asn Tyr Arg
340 345 350

Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe
355 360 365

Val Ile Gly Gly Ile Ala Met Ser Phe Ser His Gly Tyr Leu Ser Ala
370 375 380

Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg
385 390 395 400

Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr
405 410 415

Gly Gly Leu Trp Pro Val Val Ile Glu His Phe Val Asp Lys Pro Ser
420 425 430

Ile Leu

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (1)..(7)

<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,
S, OR G; X AT POSITIONS 3, 4, AND 6 ARE M, I, V,
L, F, OR Y

<400> 64

Xaa Xaa Xaa Xaa Gly Xaa Pro
1 5

<210> 65

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence between Ce orf1 and Dm orf1

<400> 65
Thr Trp Thr Phe
1

<210> 66
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence between Ce orf1 and Dm orf1

<400> 66
Gly Tyr Gly Asn
1

<210> 67
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence between Ce orf1 and Dm orf1

<400> 67
Gly Phe Gly Asp
1